

**Amendment and Response**

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For: HEPATITIS C VIRUS HELICASE CRYSTALS, CRYSTALLOGRAPHIC STRUCTURE AND METHODS

analogous portion of Hepatitis C virus helicase. Methods for generating structural information about the structurally homologous molecule or molecular complex are well-known and include, for example, molecular replacement techniques.--

Please replace the paragraph beginning at page 49, line 3, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

--The movement of domain 2 results in a change in the distance separating oligonucleotide binding sites in domain 1 and domain 2. The distance between these sites is defined as the distance between the side chain oxygen of T269 and the side chain oxygen of T411 and is tabulated for each structure in Table 7.--

**In the Claims**

Please cancel claims 1-30 and 44-46 without prejudice, amend claim 42, and add new claim 49. The new and amended claims are provided below in clean form. Per 37 C.F.R. §1.121, amended claims are also shown in Appendix A with notations to indicate changes made (for convenience, all pending claims, including those added hereby, are provided in Appendix A).

42. **(Amended)** Crystalline Hepatitis C virus helicase having amino acid sequence SEQ ID NO:1.

49. **(New)** Crystalline Hepatitis C virus helicase wherein the amino acid sequence of Hepatitis C virus helicase is SEQ ID NO:1.